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# Identification of unusual (modified and non-encoded) amino acid residues in peptides by combinations of high-performance liquid chromatography and high-performance capillary electrophoresis with matrix-assisted laser desorption ionization time-of-flight mass spectrometry

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## Abstract

The techniques for micro-level analysis of some widespread unusual amino acids (phosphorylated and hydroxylated ones) as well as of some genetically non-encoded amino acids were developed for their subsequent identification in the peptide and protein amino acid sequence by narrow-bore column high-performance liquid chromatography (~10 pmol of the sample), high-performance capillary electrophoresis (~1–10 pmol), matrix-assisted laser desorption ionization time-of-flight mass spectrometry (~1–10 pmol), and automatic protein gas phase sequencing (~1–50 pmol). © 2000 Elsevier Science B.V. All rights reserved.

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